



AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claims 1-48 (Canceled).

Claim 49 (Currently Amended): A biologically functional vector comprising a DNA sequence comprising at least ~~about 50~~ 20 consecutive nucleotides of a sequence selected from the group consisting of

- a sequence according to SEQ ID NO: 1 with an open reading frame from base pair 211 to base pair 1740, and
- a sequence which hybridizes with the sequence according to SEQ ID NO: 1 under stringent conditions,

wherein said DNA sequence is inversely oriented with respect to a promoter, and wherein said stringent conditions comprise hybridizing in a solution comprising 7% sodium dodecyl sulfate, 0.5M NaPO₄, and 1 mM EDTA at pH 7.0 and 50°C and washing with a 1% sodium dodecyl sulfate solution at 42°C.

Claim 50 (Previously Presented): A biologically functional vector comprising different length parts comprising at least 20 bases of a DNA sequence selected from the group consisting of

- a sequence according to SEQ ID NO: 1 with an open reading frame from base pair 211 to base pair 1740,

and

a sequence which hybridizes with the sequence according to SEQ ID NO: 1 under stringent conditions,

wherein said DNA sequence parts are inversely oriented with respect to a promoter, and wherein said stringent conditions comprise hybridizing in a solution comprising 7% sodium dodecyl sulfate, 0.5M NaPO₄, and 1 mM EDTA at pH 7.0 and 50°C and washing with a 1% sodium dodecyl sulfate solution at 42°C.

Claim 51 (Previously Presented): A DNA molecule coding for a ribozyme having two sequence sections,

wherein each sequence section has a length of at least 10 to 15 base pairs, and is complementary to a section of a DNA sequence selected from the group consisting of

a sequence according to SEQ ID NO: 1 with an open reading frame from base pair 211 to base pair 1740,

and

a sequence which hybridizes with the complement of the sequence according to SEQ ID NO 1 under stringent conditions,

wherein said ribozyme complexes and cuts the mRNA transcribed by a natural GlcNAc- α 1,3-fucosyl transferase DNA molecule, and wherein said stringent conditions comprise hybridizing in a solution comprising 7% sodium dodecyl sulfate, 0.5M NaPO₄, and 1 mM EDTA at pH 7.0 and 50°C and washing with a 1% sodium dodecyl sulfate solution at 42°C.

Claim 52 (Previously Presented): A biologically functional vector comprising said DNA molecule according to claim 51.

Claims 53-56 (Canceled)

Claim 57 (Previously Presented): A method of preparing recombinant hosts selected from the group consisting of host cells, plant cells, insect cells, plants and insects wherein the production of GlcNAc- α -1,3-fucosyl transferase is suppressed or inhibited, comprising identifying a DNA sequence in a host that codes for a protein having fucosyl transferase activity, said sequence comprising a DNA sequence selected from the group consisting of

(A) a sequence according to SEQ ID NO: 1 with an open reading frame from base pair 211 to base pair 1740,

(B) a sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1, and

(C) a sequence which hybridizes with the sequence according to SEQ ID NO: 1 under stringent conditions,

and inserting into said host a biologically functional vector comprising at least 20 bases of the identified DNA sequence inversely oriented with respect to a promoter,

wherein said stringent conditions comprise hybridizing in a solution comprising 7% sodium dodecyl sulfate, 0.5M NaPO₄, and 1 mM EDTA at pH 7.0 and 50°C and washing with a 1% sodium dodecyl sulfate solution at 42°C.

Claim 58 (Previously Presented): A method of preparing recombinant hosts selected from the group consisting of host cells, plant cells, insect cells, plants and insects wherein the production of GlcNAc- α -1,3-fucosyl transferase is suppressed or inhibited, comprising

identifying a DNA sequence in a host that codes for a protein having fucosyl transferase activity, said sequence comprising a sequence selected from the group consisting of

(A) a sequence according to SEQ ID NO: 1 with an open reading frame from base pair 211 to base pair 1740,

(B) a sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1, and

(C) a sequence which hybridizes with the sequence according to SEQ ID NO: 1 under stringent conditions,

and, inserting into said host, a biologically functional vector which comprises parts of the identified DNA sequence said parts having at least 20 base pairs, wherein said DNA sequence is inversely oriented with respect to a promoter,

and wherein said stringent conditions comprise hybridizing in a solution comprising 7% sodium dodecyl sulfate, 0.5M NaPO₄, and 1 mM EDTA at pH 7.0 and 50°C and washing with a 1% sodium dodecyl sulfate solution at 42°C.

Claim 59 (Canceled).

Claim 60 (Previously Presented): A method of preparing recombinant hosts selected from the group consisting of host cells, plant cells, insect cells, plant tissues, plants and

insects wherein the production of GlcNAc- α -1,3-fucosyl transferase is suppressed or inhibited, comprising

inserting into a recombinant host, a biologically functional vector which comprises a DNA molecule according to claim 51.

Claim 61 (Previously Presented): A method of preparing recombinant hosts selected from the group consisting of host cells, plant cells, insect cells, plant tissues, plants and insects, comprising

identifying in the genome of a host, a non-mutated sequence that codes for a protein having fucosyl transferase activity wherein the non-mutated sequence comprises a sequence selected from the group consisting of

(A) a sequence according to SEQ ID NO: 1 with an open reading frame from base pair 211 to base pair 1740,

(B) a sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1, and

(C) a sequence which hybridizes with the sequence according to SEQ ID NO: 1 under stringent conditions, and

inserting a homologous DNA molecule into the genome of said host at the position of said non-mutated sequence, said DNA molecule comprising all or part of said identified sequence except for having a deletion, insertion or substitution mutation,

and wherein said stringent conditions comprise hybridizing in a solution comprising 7% sodium dodecyl sulfate, 0.5M NaPO₄, and 1 mM EDTA at pH 7.0 and 50°C and washing with a 1% sodium dodecyl sulfate solution at 42°C.

Claim 62 (Previously Presented): A recombinant host prepared according to said method according to claim 60, wherein its GlcNAc- α 1,3-fucosyl transferase production is suppressed.

Claim 63 (Previously Presented): A recombinant host prepared according to said method according to claim 60, wherein its GlcNAc- α 1,3-fucosyl transferase production is completely inhibited.

Claims 64-75 (Canceled).

Claim 76 (Previously Presented): A method of producing recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 62, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 77 (Previously Presented): A method of producing recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 63, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claims 78-82 (Canceled).

Claim 83 (Previously Presented): A method of producing human recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 62, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 84 (Previously Presented). A method of producing human recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 63, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claims 85-107 (Canceled).

Claim 108 (Previously Presented): A recombinant host prepared according to claim 57, wherein its GlcNAc- α 1,3-fucosyl transferase production is suppressed.

Claim 109 (Previously Presented): A recombinant host prepared according to claim 57, wherein its GlcNAc- α 1,3-fucosyl transferase production is completely inhibited.

Claim 110 (Previously Presented): A recombinant host prepared according to claim 58, wherein its GlcNAc- α 1,3-fucosyl transferase production is suppressed.

Claim 111 (Previously Presented): A recombinant host prepared according to claim 58, wherein its GlcNAc- α 1,3-fucosyl transferase production is completely inhibited.

Claim 112 (Previously Presented): A method of producing recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 108, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 113 (Previously Presented): A method of producing recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 109, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 114 (Previously Presented): A method of producing recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 110, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 115 (Previously Presented): A method of producing recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 111, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 116 (Previously Presented): A method of producing human recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 108, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 117 (Previously Presented): A method of producing human recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 109, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 118 (Previously Presented): A method of producing human recombinant glycoprotein, comprising
transfecting a recombinant host according to claim 110, with a gene that expresses said glycoprotein, and
expressing said recombinant glycoprotein.

Claim 119 (Previously Presented): A method of producing human recombinant glycoprotein, comprising

transfecting a recombinant host according to claim 111, with a gene that expresses said glycoprotein, and

expressing said recombinant glycoprotein.

Claim 120 (Currently Amended): A biologically functional vector comprising a DNA sequence comprising at least ~~about 50~~ 20 consecutive nucleotides of a sequence that is at least 50% homologous with the sequence according to SEQ ID NO: 1 and that encodes a plant protein having fucosyl transferase activity, wherein said DNA sequence is inversely oriented with respect to a promoter.

Claim 121 (Previously Presented): A biologically functional vector comprising different length parts comprising at least 20 bases of a DNA sequence that is at least 50% homologous with the sequence according to SEQ ID NO: 1 and that encodes a plant protein having fucosyl transferase activity, wherein said DNA sequence is inversely oriented with respect to a promoter.

Claim 122 (Previously Presented): A DNA molecule coding for a ribozyme having two sequence sections, wherein each sequence section has a length of at least 10 to 15 base pairs, and is complementary to a section of a DNA sequence that is at least 50% homologous to the sequence according to SEQ ID NO: 1 and that encodes a plant protein having fucosyl transferase activity, wherein said ribozyme complexes and cuts the mRNA transcribed by a natural GlcNAc- α 1,3-fucosyl transferase DNA molecule.

Claim 123 (Previously Presented): A biologically functional vector comprising said DNA molecule according to claim 122.

Claim 124 (New) The method of claim 57, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 70% to 80% homologous with the sequence according to SEQ ID NO 1.

Claim 125 (New) The method of claim 57, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 95% homologous with the sequence according to SEQ ID NO 1.

Claim 126 (New) The method of claim 58, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 70% to 80% homologous with the sequence according to SEQ ID NO 1.

Claim 127 (New) The method of claim 58, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 95% homologous with the sequence according to SEQ ID NO 1.

Claim 128 (New) The method of claim 61, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 70% to 80% homologous with the sequence according to SEQ ID NO 1.

Claim 129 (New) The method of claim 61, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 95% homologous with the sequence according to SEQ ID NO 1.

Claim 130 (New) The vector of claim 120, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 70% to 80% homologous with the sequence according to SEQ ID NO 1.

Claim 131 (New) The vector of claim 120, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 95% homologous with the sequence according to SEQ ID NO 1.

Claim 132 (New) The vector of claim 121, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 70% to 80% homologous with the sequence according to SEQ ID NO 1.

Claim 133 (New) The vector of claim 121, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 95% homologous with the sequence according to SEQ ID NO 1.

Claim 134 (New) The vector of claim 122, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 70% to 80% homologous with the sequence according to SEQ ID NO 1.

Claim 135 (New) The vector of claim 122, wherein the sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1 is a sequence that is at least 95% homologous with the sequence according to SEQ ID NO 1.